

31 ATGGCAACAGCTGAGGAATCGAACGCCATCGAATGGCCACCGCCACAGTACGCTCCTGGAAGAGCTGTGCCACAGC
 1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
 91 GAGACGCCGCACTGGAGCCCAAGCGAGCAAAACAGCCCATAGACAAGCCCATCTGCGCCACCTGAGCCAACTGAGCCACCTG
 31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
 181 CTCATCATCGCCGACTGTGATCGTCTGTGTTGGCGGCGTGACGGAGGGCCGCGGCATGGCGCTCATGTTTCGAGGAGTCCGACACG
 61 L I I A G L L I V C L A G V T E G R R H A P L M F E S D T
 271 GGCAGGCGGTCCAACCGACCGGTCAACCGAATGCCAGTTTGGCAAGTTTGGCGGAATGGGTCCACCTGGTATGCGGATTGGGT
 91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
 361 CCACCTTCGGAGTTATGTAATCAAGTGTGAATGTGCGCATACCAAGAGCGGCGCATCGTTGCACGCGTCCAGTGTGCAAT
 121 P P F G V M Y C I K C E C V A I P K R R I V A R V Q C R N
 451 ATCAAAACGAGTGCCTGGCGGCAAAATGCGATGATCCCATCTCGTTGGCGGAAATGCTGCAAGACCTGTCCCGCGCATCGAAACGAT
 151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
 541 ACGATGTAGCCTTGGATGTGCCGTGCCCAATGAAGAGGAAGAGCGCAACATGAACAATTACGCTGCGTTGCTAACGGCGCACCTCC
 181 T D V A L D V P V P N E E E E R N M K H Y A A L L T G R T S
 631 TATTTCTCAAGGTGAGGAATGAAGTCCATGTACACCACTACAATCGGCAAGATCTGGTGGCCACCGCCCGTTCTCTGTTCCACAAG
 211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
 721 AAGAATCTATCTACTCTTACACCTCATCGGAATCGGTCTCGCGTGCATTCAATTCGTTGATGATCGGGTGTAACTCTGGAG
 241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
 811 GAGCATCAACTGGAGACCCTTGGCGGCACTCTCAGTGTCTATCAGAATGCCACGGCAAGATCTGA
 271 E H Q L E T T L A G T L S V Y A N A T G K I STOP

FIGURE 1

1 ATGGCCAAAGCTGAGGAATCGAAGCCCATCGAATGGGCCACGGCCACAGTACCGCTCTCTGGAAGGAGCTGTGCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
91 GAGGACGGCGACTGGAGCCCAAGCGAGCAAAACACAGCCATAGAGAACAGCCCCCATCTCGCGCCACCTGAGCCACCTG
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
181 CTATCATCGCGGACTGTGATCGTCTGTGGCGGCGTACGAGGGCGCGGCATGCGCGCTCATGTCGAGGAGTCCGACACG
61 L I I A G L L I V C L A G V T E G R R H A P L M F E S D T
271 GCGAGGGGTCCAACGACGAGCGGTCAACGAATGCCAGTTTGGCAAATTTGGGTCACCTGGTATGCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T M Y A D L G
361 CCACCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGCGCATACCCAAAGAGCGCGCATCGTTGCACGCTCCAGTGTCCGAAT
121 P P F G V M Y C I K C E C V A I P K R R I V A R V Q C R N
451 ATCAAACGAGTCCCGCGGCAAAATGGATGATCCCTCTGTGTCGCGGAAATGTGCAAGACCTGTCCGCGCATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
541 ACGGATGTAGCTTGGATGTGCCCGTCCCAATGAAGAGGAGCGCAACATGAACATTACGTCGCTTGTACGGGCGCGCACCTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S
631 TATTTCTCAAGGTGAGGAAATGAAGTCCATGTACACCACTACAATCCGAGAACTGTGTGGCCACCGCCCGTTCTCTGTTCCACAAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
721 AAGAATCTACTACTCTTCTACACCTCATCGCAATCGTCTGTCGCGTCCATTCAATTCGTTGATGATCGGGGTGTAATCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
811 GAGCATCAACTGGAGACCACTTGGCGGCACTCTCAGTGTCTATCAGATGCCAGGCAAGATCGGCGCGGTCTCGAGGTACTCTTA
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L
901 GAGGATCTTCTGAAGGACCTTACTTCTGTCGTGACATAATGGACAAACTACCTACAGAGATTTAAGCTCTAA
301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

TM
CRI
pLIAS
Sequences

FIGURE 2

1 ATGCCAACAAAGCTGAGGAAATCGAAATGGGCCACGGCCACGGCACAGTACCGCTCTCGAAAGGAGCTCTGCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S

91 GAGGACGGCGCACTGGAGCCCAAGCGAGCAAAACAGCATAGAGAAACAAGCCCACTCTGGCCCACTGAGCCAACTGAGCCACCTG
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L

181 CTGATCGCCGAGCTGCTGATGCTGCTTGGCGGGGTGAGGAGGGCGCGGCATGCGCGCTCATGTTGAGGAGTCCGACACG
61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T

271 GGCAGGCGGTCCAAACCGACCGGTACCGAATGCCAGTTTGGCAAATTTGCGGAATTTGGGGTCCACCTGGTATGCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G

361 CCACCTTCGGAGTTATGCTACTGTCATCAAGTGTGAATGTGTGCGCATACCCAAAGAGCGGGCGCATCGTTGCACGCTCCAGTGTGCGCAT
121 P P F G V M Y C I K C E C V A I P K K R R I V A R V Q C R N

451 ATCAAAACGAGTCCCGCGGCAAAATGCGATGCCATCTGTTGCCGGAATGCTGCAAGACCTGTCCCGCGCATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D

541 ACGGATGTAGCCTTGGATGTGCCCGTCCCAATGAAGAGAGAGCGCAACATGAACATTTAGCTGCGTTGCTAACGGGCGCGCACCTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S

631 TATTTCTCAAGGGTGAGGAAATGAAGTCCATGTACACCACTTACAAATCCGAGAAATCTGTGGCCACCGCGTTTCTGTTCCACAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K

721 AAGAATCTATCTCTACACCTCATCGGGAATCGGTGCTCGCGTGCCCAATTCATTCGTTGATGATGCGGGTGTAACTCTGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E

811 GAGCATCAACTGGAGACCACTTGGCGGCACTCTCAGTGTCTATCAGAATGCCACGGGCAAGATCGCCCGGCTCGAGGTACCTCTA
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R V P L

901 GAGGATCTTTGTGAAGAACCTTACTTCTGTGGTGTGACATAAATTGGACAACTACTCTACAGAGATTTAAAGCTCTAA
301 E D L C E G T L L L W C D I I G N T T Y R D L K L STOP

TM

CRI:W->A

pUAS
Sequences

FIGURE 3

1 ATGGCCAACAAGCTGAGGAAATCGAACGCCATCGAATGGGCACGGCCACGGCACAGTACCGCTCTCTGGAAGGAGCTGCTCCACAGC
1 M A N K L R K S N A I E W A T A T G T V P L L E R S C C H S
91 GAGGACGCCGCACTGGAGCCCCAAGCAGACGAAACCCAGCCATAGAACCAAGCCCGCATCTGCGCACCTGAGCCAACTGAGCCACCTG TM
31 E D A A L E P Q A S K T S H R E Q A P I L R H L S Q L S H L
181 CTCATCATCGCCGACTGCTGCTGCTGGCGGGCTGACGGAGGGCGCCGCGCATGGRHAPLMFEEST
61 L I I A G L L I V C L A G V T E G R R H A P L M F E E S D T
271 GCGAGCGGTCCACCGACCGGTCCACCGAATGCCAGTTTGGCAAGTTTGGCGAATTGGGTCCACCTGGTATCGGATTTGGGT
91 G R R S N R P A V T E C Q F G K V L R E L G S T W Y A D L G
361 CCACCTTCGGAGTTATGTACTGCATCAAGTGTGAATGTGTGCGCATACCAAGAGCGCGCATCGTTGACCGCTCCAGTGTGCGCAAT
121 P P F G V M Y C I K C E C V A I P K R R I V A R V Q C R N
451 ATCAAACGAGTGCCTGGCGGCAAAATGCGATGATCCCATCTCTGTCGCGGAAATGTGCAAGACCTGTCGCGCATCGAAACGAT
151 I K N E C P P A K C D D P I S L P G K C C K T C P G D R N D
541 ACGGATGTAGCCTTGGATGTGCCGTGCCCAATGAGAGGAAGCGCAACATGAAACATTACGCTGCGTTGCTAACGGCGCGCACTCC
181 T D V A L D V P V P N E E E R N M K H Y A A L L T G R T S
631 TATTTCTCAAGGTTGAGGAAATGAAGTCCATGTACACCACTACAATCGCAGAAATCTGGTGGCCACCGCCGTTTCTCTTCCACAAG
211 Y F L K G E E M K S M Y T T Y N P Q N V V A T A R F L F H K
721 AAGAATCTATACTACTCTTCTACACCTCATCGGAATCGGTGCTCGGTGCCATTCAATTCTGTTGATGCGGGTGTAAATCCTGGAG
241 K N L Y Y S F Y T S S R I G R P R A I Q F V D D A G V I L E
811 GAGCATCAACTGGAGACCACTTGGCGGCACTCTCAGTCTCTATCAGAAATGCCAGGCAAGATCGGCCGGCTCGAGGCGAGCGCGG
271 E H Q L E T T L A G T L S V Y A N A T G K I G R G S R N R G PUAS/PCR
901 CGCATCTTTACCCATACGATGTTCTGACTATGGGGCTATCCCTATCAGTCCCGGACTATGACGATCTCTATCCATATGACCTTCCA
301 R I F Y P Y D V F D Y A G Y P Y D V P D Y A G S Y P Y D V P
991 GATTACGCTGCTCAGTGGCGCGATTATACGGACGACGACGACAAATCA
331 D Y A A N C G R D Y K D D D K stop

SX-HA
IX-FLAG

FIGURE 4

	10	20	30	40	50	60	70
Nog protei	MDHSQCLVTIYALMVFGLGRIDQGCGHYLHIRPAPSENLPVLDLIEHPDPIYDPKEKDLNETLLRTLMVGHFDP						
SuperSog P [71]	<hr/>						
	260	270	280				
	iqfvdagvile--EhqletTLaGTLSv--ygn						
	AAAAAAAAVV^	^-----^VV^V^	^				
Nog protei	VDLIEHPDPIYDPKEKDLNETLLRTLMVGHFDP						

	90	* 100	110	120	130	140	150
Nog protei	I L P E E R L G V E D I G E L D L L L R Q K P S G A M P A E I N G K L F Y E G L O S K K H R L S K K L R R K L Q M L W S Q T F C P V L Y T W N D L G						
SuperSog P (71)			300	310	P U A S Vector		
		I g x s r v p l e d l c e g t l l l w >					
		v - - - ^ ^ ^ ^ ^ v - ^ ^ ^ ^					
Nog protei	I L P E E R L G V E D I G E L D L L L R						

Nog protei

FIGURE 5

